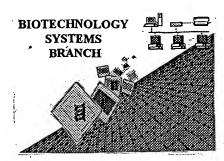


## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/024, 036
Source: 01/15/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.1 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

- 1. EFS-Bio (<a href="http://www.uspto.gov/ebc/efs/downloads/documents.htm">http://www.uspto.gov/ebc/efs/downloads/documents.htm</a>, EFS Submission User Manual ePAVE)
- 2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
- Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
  - U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
- Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

## Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 10/024,036										
CRRORE	THE PROPERTY OF THE PROPERTY O										
ATTN: NEW RULES CASES:	PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE										
1Wrapped Nucleics Wrapped Aminos	ne number/text at the end of each line "wrapped" down to the next line. This may occur if your file as retrieved in a word processor after creating it. Please adjust your right margin to .3; this will event "wrapping."										
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.										
3Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.										
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.										
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.										
6PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.										
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  This sequence is intentionally skipped										
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.										
8Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000										
9 Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing.  Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.										
10Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence										
11Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or  "Unknown." Please explain source of genetic material in <220> to <223> section.  (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)										
PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.										
13Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.										

AMC/MH - Biotechnology Systems Branch - 08/21/2001

OIPE

RAW SEQUENCE LISTING DATE: 01/15/2002 PATENT APPLICATION: US/10/024,036 TIME: 18:18:40

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Output Set: N:\CRF3\01152002\J024036.raw

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                                                                  see p.S, Lod
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  10 <130> FILE REFERENCE: MPI2000-521P1R(M)
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  44 Pro Arg Arg Ala Pro Gly Ala Pro Ser Pro Ala Arg Pro Arg Pro Leu
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  45
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  48 Leu Arg Ala Ala Leu Val Gly His Gly Pro Gly Glu Arg Arg Glu Gln
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  52 Leu Leu Glu Lys Ala Ser * Arg His Gln Glu Asp Leu Arg Val
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/024,036

DATE: 01/15/2002
TIME: 18:18:40

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Output Set: N:\CRF3\01152002\J024036.raw

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92 Lys Asn Gly Gly Gln Arg Arg 220 93 215 220 95 agg cta tgt cgc tcc tga agt cct cgc cca gaa acc tta cag caa agc 770 96 Arg Leu Cys Arg Ser * Ser Pro Arg Pro Glu Thr Leu Gln Gln Ser 97 230 99 cgt tga ctg ctg gtc cat cgg agt gat tgc cta cat ctt gct ctg cgg 818 100 Arg * Leu Leu Val His Arg Ser Asp Cys Leu His Leu Ala Leu Arg 250 101 245 103 cta ccc tcc ttt tta tga tga aaa tga ctc caa gct ctt tga gca gat 104 Leu Pro Ser Phe Leu * * Lys * Leu Gln Ala Leu * Ala Asp 265 107 cct caa ggc gga ata tga gtt tga ctc tcc cta ctg gga tga cat ctc 108 Pro Gln Gly Gly Ile * Val * Leu Ser Leu Leu Gly * His Leu 110 Pro Glu 275 111 cga ctc tgc aaa aga ctt cat tcg gaa cct gat gga gaa gga ccc gaa 112 Arg Leu Cys Lys Arg Leu His Ser Glu Pro Asp Gly Glu Gly Pro Glu 119 tga cac agc cct caa caa aaa cat cca cga gtc gga cac cag cgc cag at 100 119 tga cac agc cct caa caa aaa cat cca cga gtc ggc aga cag cgc cgc aga aaa ctt taa tgc cac 110 110 110 110 110 110 110 110 110 11	of aga gag ggg caa agg aga tgt gat gtc cac tgc ctg tgg das	Ser
95 agg cta tgt cgc tcc tga agt cct cgc cca gaa acc tta cag caa agc	02 Two Ash Gly GIV GIN AIG AIG CIS INF	
95 agg cta tgt cgc tcc tga agt cct cgc cca gaa acc tta cdg cdg system of the leu Cys Arg Ser * Ser Pro Arg Pro Glu Thr Leu Gln Gln Ser 230 99 cgt tga ctg ctg gtc cat cgg agt gat tgc cta cat ctt gct ctg cgg 99 cgt tga ctg ctg gtc cat cgg agt gat tgc cta cat ctt gct ctg cgg 100 Arg * Leu Leu Val His Arg Ser Asp Cys Leu His Leu Ala Leu Arg 250 101 245 103 cta ccc tcc ttt tta tga tga aaa tga ctc caa gct ctt tga gca gat 104 Leu Pro Ser Phe Leu * * Lys * Leu Gln Ala Leu * Ala Asp 265 105 260 107 cct caa ggc gga ata tga gtt tga ctc tcc cta ctg gga tga cat ctc 107 cct caa ggc gga ata tga gtt tga ctc tcc cta ctg gga tga cat ctc 108 Pro Gln Gly Gly Ile * Val * Leu Ser Leu Leu Gly * His Leu 109 109 275 111 cga ctc tgc aaa aga ctt cat tcg gaa cct gat gga gaa gga ccc gaa 112 Arg Leu Cys Lys Arg Leu His Ser Glu Pro Asp Gly Glu Gly Pro Glu 112 Arg Leu Cys Lys Arg Leu His Ser Glu Pro Asp Gly Glu Gly Pro Glu 116 * Lys Ile His Val * Ala Gly Ser Ser Ala Pro Met Asp Arg Trp 116 * Lys Ile His Val * Ala Gly Ser Ser Ala Pro Met Asp Arg Trp 117 300 119 tga cac agc cct caa caa aaa cat cca cga gtc cgt cag cgc cca gat 1010 119 tga cac agc cct caa caa aaa cat cca cga gtc cgt cag cgc cca gat 1010 110 * His Ser Pro Gln Gln Lys His Pro Arg Val Arg Gln Arg Pro Asp 120	220	agc 770
96 Arg Leu Cys Arg Ser	of agg cta tgt cgc tcc tga agt cct cgc cca gaa acc tta cay cua	~ 3 ~
97	of Arg Lou Cys Arg Ser * Ser Pro Arg Pro Glu Thr Leu Gin Gin	501
100 Arg	235 240	cgg 818
100 Arg	on agt tgg ctg ctg gtc cat cgg agt gat tgc cta cat ctt gct ctg	ıΔrα
101	100 Arg. * Leu Vel His Arg Ser Asp Cys Leu His Leu Ald Leu	u nry
104 Leu Pro Ser Phe Leu   265   270	100 Arg 255	a gat 866
104 Leu Pro Ser Phe Leu   265   270	101 102 eta con toc ttt tta tga tga aaa tga ctc caa gct ctt tga gct	a Agn
105	104 For Dro Ser Phe Leu " " " " " " " " " " " " " " " " " " "	270
108 Pro Gln Gly Gly 11e	104 Let 110 Set 110 = 265	+ c+c 914
108 Pro Gln Gly Gly 11e	103 and gas and gas ata that the ctc too cta ctg gga the things and the things are the case and the case are the case and the case are the cas	c Tell
111 cga ctc tgc aaa aga ctt cat tcg gaa cct gat gga gaa gga ccc gaa 1010  112 Arg Leu Cys Lys Arg Leu His Ser Glu Pro Asp Gly Glu Gly Pro Glu 295  113	107 CCt Caa ggo gga Lee * Val * Leu Ser Leu Leu Gly * HIS	5 Hea
111 cga ctc tgc aaa aga ctt cat tcg gaa cct gat gga gaa gga gga gga gga gga gga gg	108 PIO GIR GII GII 275	962
112 Arg Leu Cys Lys Arg Leu His Sol	109	
113	111 cga ctc tgc dad ay	O GIU
116 * Lys IIe His Val	112 Arg Led Cys Lys 11-5 - 295	-a +aa 1010
116 * Lys IIe His Val	113 203 at a cac gtg tga gca ggc agc tcg gca ccc atg gat cg	ic tyg 1010
117 300  119 tga cac agc cct caa caa aaa cat cca cga gtc cgt cag cgc cca gat  119 tga cac agc cct caa caa aaa cat cca cga gtc cgt cag cgc cca gat  120 * His Ser Pro Gln Gln Lys His Pro Arg Val Arg Gln Arg Pro Asp  121 315 320 325  122 ccg gaa aaa ctt tgc caa gag caa atg gag aca agc att taa tgc cac  123 ccg gaa aaa ctt tgc caa gag caa atg gag aca agc att taa tgc cac  124 Pro Glu Lys Leu Cys Gln Glu Gln Met Glu Thr Ser Ile * Cys His  125 330 335  127 ggc cgt cgt gag aca tat gag aaa act aca cct cgg cag cag cct gga  128 Gly Arg Arg Glu Thr Tyr Glu Lys Thr Thr Pro Arg Gln Gln Pro Gly  129 345	115 tad add atd dds 353 * Ala Gly Ser Ser Ala Pro Met ASP Al	.g 11P
120 * His Ser Pro Gin Gin Lys His 120 325  121 315 320 320  123 ccg gaa aaa ctt tgc caa gag caa atg gag aca agc att taa tgc cac 1106  123 ccg gaa aaa ctt tgc caa gag caa atg gag aca agc att taa tgc cac 1106  124 Pro Glu Lys Leu Cys Gln Glu Gln Met Glu Thr Ser Ile * Cys His 340  125 330 335 340  127 ggc cgt cgt gag aca tat gag aaa act aca cct cgg cag cag cct gga 1154  127 ggc cgt cgt gag aca tat gag aaa act aca cct cgg cag cag cct gga 1154  128 Gly Arg Arg Glu Thr Tyr Glu Lys Thr Thr Pro Arg Gln Gln Pro Gly 355  129 345	305	1058
120 * His Ser Pro Gin Gin Lys His 120 325  121 315 320 320  123 ccg gaa aaa ctt tgc caa gag caa atg gag aca agc att taa tgc cac 1106  123 ccg gaa aaa ctt tgc caa gag caa atg gag aca agc att taa tgc cac 1106  124 Pro Glu Lys Leu Cys Gln Glu Gln Met Glu Thr Ser Ile * Cys His 340  125 330 335 340  127 ggc cgt cgt gag aca tat gag aaa act aca cct cgg cag cag cct gga 1154  127 ggc cgt cgt gag aca tat gag aaa act aca cct cgg cag cag cct gga 1154  128 Gly Arg Arg Glu Thr Tyr Glu Lys Thr Thr Pro Arg Gln Gln Pro Gly 355  129 345	117 300 and cat caa caa aaa cat cca cga gtc cgt cag cgc cc	sa yac 1000
121 315 123 ccg gaa aaa ctt tgc caa gag caa atg gag aca agc att taa tgc cac 1106 123 ccg gaa aaa ctt tgc caa gag caa atg gag aca agc att taa tgc cac 1106 124 Pro Glu Lys Leu Cys Gln Glu Gln Met Glu Thr Ser Ile * Cys His 125 330 335 340 127 ggc cgt cgt gag aca tat gag aaa act aca cct cgg cag cag cct gga 1154 128 Gly Arg Arg Glu Thr Tyr Glu Lys Thr Thr Pro Arg Gln Gln Pro Gly 128 Gly Arg Arg Glu Thr Tyr Glu Lys Thr Thr Pro Arg Gln Gln Pro Gly 129 345	119 tga cac age cee can but his Pro Arg Val Arg Gln Arg Pr	ro Asp
121 S13 Ccg gaa aaa ctt tgc caa gag caa atg gag aca agc att taa tgc cac 1100 123 ccg gaa aaa ctt tgc Caa gag caa atg gag aca agc att taa tgc Cac 1100 124 Pro Glu Lys Leu Cys Gln Glu Gln Met Glu Thr Ser Ile * Cys His 340 125 330 335 340 127 ggc cgt cgt gag aca tat gag aaa act aca cct cgg cag cag cct gga 1154 127 ggc cgt cgt gag aca tat gag aaa act aca cct cgg cag cag cct gga 1154 128 Gly Arg Arg Glu Thr Tyr Glu Lys Thr Thr Pro Arg Gln Gln Pro Gly 355 350 350 350 350 350 350 350	120 * His Sel Plo din dan -1 320	1106
124 Pro Glu Lys Leu Cys Gli Glu Sia 340 125 330 335 340 127 ggc cgt cgt gag aca tat gag aaa act aca cct cgg cag cag cct gga 1154 127 ggc cgt cgt gag aca tat gag aaa act aca cct cgg cag cag cct gga 1154 128 Gly Arg Arg Glu Thr Tyr Glu Lys Thr Thr Pro Arg Gln Gln Pro Gly 128 Gly Arg Arg Glu Thr Tyr Glu Lys Thr Thr Pro Arg Gln Gln Pro Gly 355 129 345	121 $313$ $313$ $313$ $313$ $313$ $313$ $313$ $313$ $313$ $313$ $313$ $313$ $313$ $313$	gc cac 1100
125 330  127 ggc cgt cgt gag aca tat gag aaa act aca cct cgg cag cag cct gga  127 ggc cgt cgt gag aca tat gag aaa act aca cct cgg cag cag cct gga  128 Gly Arg Arg Glu Thr Tyr Glu Lys Thr Thr Pro Arg Gln Gln Pro Gly  355  129 345	123 ccg gaa aad ctt tye caa gay	ys H1S
125 330  127 ggc cgt cgt gag aca tat gag aaa act aca cct cgg cag cag cct gga  127 ggc cgt cgt gag aca tat gag aaa act aca cct cgg cag cag cct gga  128 Gly Arg Arg Glu Thr Tyr Glu Lys Thr Thr Pro Arg Gln Gln Pro Gly  355  129 345	124 Pro Glu Lys Leu Cys off 335	1154
128 Gly Arg Arg Glu Thr Tyl Glu Lys 128 355 350 350 355 227 cet cag ttt ggc cag cca aaa 1202	125 330 and against ag	ct gga 1134
129 345	127 ggc cgt cgt gag aca the gag and Thr Thr Pro Arg Gln Gln Pr	ro Gly
129 345	128 Gly Arg Arg Glu IIII 191 Glu 275 350 355	1000
131 cag ttc aaa tgc aag tgt ttc gag oag trouble Gly Gln Pro Lys	129 345	ca aaa 1202
122 Cln Phe Lvs Cvs Lys Cys File Old Old	131 cag ttc aaa tgc aay tyc ttc gay our Pro Gln Phe Gly Gln Pro	ro Lys
132 GIII INC 110 01- 1 -	132 Gln Phe Lys Cys Lys Cys Phe Gra Gra	٠.

DATE: 01/15/2002 RAW SEQUENCE LISTING TIME: 18:18:40 PATENT APPLICATION: US/10/024,036

Input Set : A:\seq list.txt

Output Set: N:\CRF3\01152002\J024036.raw

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122	260				7	365				3	370					375	
133	- ~ -	ota i	tac (	rta i	tat a	age a	aaa a	acc a	aga a	atc o	cct	cag	ctg a	a cad	ctgaa	agac	1252
133	aya Arg	CLY 1	CTTC T	7=1 (	772	Ser 1	īvs '	rhr i	Arq :	Ile 1	Pro	Gln :	Leu				
137			~~ +			י ממי	addd	адса	tct	acca	agc	acct	cctg	tt to	gcca	ggcgc	1312 1372
141 geoggetgea gtggeteaeg eetglaatee taacateteg ggtgaaacce catetetaet 1492 142 tgtttgagtt caggagtttt aagaccagee tgaccaacat ggtgaaacce catetetaet 1492 143 aaaatataaa aattageegg gtgtggtgge gagcacetgt aatgteaget acttgggagg 1552																	
144 ctgaggcagg agaatcactt gaacccagga agcggaggtt gcaatgaget gagaatca 1672 145 cactgcactc cagcctgggt gacagattga gactccctct caaaaaaaaa agggaaatca 1672												1672					
145	cact	gcac	tc c	agcc	tggg	i ya	caya ~+~+	-cega	+ = +	toca	+++	acaa	t.t.t.a	σσ a	atcc	agggc	1732 1772
146	ttga	acac	tc g	tgga	accc	t ag	giai	cyca	ata	ntaa	tca	4099		,,			1772
147	tcaa	ıgtcc	tc g	cagg	ggta	c cg	agei	cyay	acc	y caa	LCu						
149	<210	)> SE	Q ID	NO:	2												
	<211				8												
151	<212	2> TY	PE:	PRT													
152	<213	3> OR	GANI	SM:	Huma	n											
154	<400	)> SE	QUEN	CE:	2	_		_		T	T 011	Cln	λκα	Δτα	Lvs	Leu	
155	Arg	Arg	Arg	Ala	His	Glu	Arg	гàг	Arg	тур	ьeu	GIII	Arg	nrg	15	200	
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157	Arg	Arg	Ser	Pro	Ser	Arg	Pro	Ala	ser	Pro	PIO	PIO	пец	30	110		
4 = 0				20					25					50			
159	Arg	Ala	Pro	Gly	Ala	Pro	Ser	Pro	Ala	Arg	Pro	Arg	15	пец	пси	1119	
			2 E					40					43				
161	Ala	Ala	Leu	Val	Gly	His	Gly	Pro	Gly	Glu	Arg	Arg	GIU	GIII	пец	пеа	
		_ ^					רר					UU					
163	Leu	Glu	Lys	Ala	Ser	Arg	His	Gln	Glu	Asp	Leu	Arg	vaı	GIII	ALG	80	
						70					13					-	
165	65 Pro	Arg	Asn	Arg	Gly	Leu	Phe	Arg	Ser	Gly	Phe	ser	arg	GIU	95	ASII	
					0 5					90							
167	Trp	Gln	Ala	Leu	Cys	Cys	Glu	Val	Tyr	Pro	GLu	GTĀ	Ala	110	СТУ	GIII	
200				100					TOO					110			
169	s Gly	Lys	Gln	His	Arg	Glu	Asp	ser	Arg	Pro	Glu	Lys	Asp	Ala	гуѕ	тут	
			115					120					127				
171	) L Cys	Cys	Pro	Gly	Arg	His	Leu	Lys	Pro	Lys	Ser	Pro	Val	Leu	GTĀ	HIS	
		4 2 2					1135					T40					
173	2 3 Ala	Ala	Gly	Val	Arg	Trp	Arg	Ala	Val	Pro	Asp	Ser	GLY	GIU	GIY	Val	
4 -						150					エンン						
1.7	1 145 5 Leu	Tyr	Arg	Glu	Gly	Cys	Gln	His	ser	Asp	Pro	Pro	Ser	ьeu	GIY	ALG	
17	_				165					T/0					1,0		
17	o 7 Arg	val	Leu	Ser	Pro	Gln	Asn	Gly	His	Arg	Pro	Gln	Arg	Pro	GIn	Ala	
4	_			100					เหว					100			
17	s 9 Arg	Lvs	Ser	Leu	Va1	Leu	Gln	Ser	Arg	Gly	Val	. Gln	Asn	Asn	Asp	GID	
	_		105					- 200					200				
18	u 1 Leu	n Trn	Ile	Val	Lys	Asn	Gly	Gly	Gln	Arg	Arg	y Cys	Asp	Val	His	Cys	
10	^	210					215					220					
1Ω	<u>د</u> ۲.۵۱۰	፲፲ ፲ ጥጥካ	Asn	Ser	Ara	Leu	Cys	Arg	ser	Ser	Pro	Arg	Pro	Glu	Thr	Leu 240	
10	4 225	:				- 230					45.	,					
10	5 61r	r Cln	Ser	Ara	Leu	Leu	Val	His	Arg	Ser	Asp	Cys	Leu	His	Leu	Ala	
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DATE: 01/15/2002 RAW SEQUENCE LISTING TIME: 18:18:40 PATENT APPLICATION: US/10/024,036

Input Set : A:\seq list.txt

Output Set: N:\CRF3\01152002\J024036.raw

```
255
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187 Leu Arg Leu Pro Ser Phe Leu Lys Leu Gln Ala Leu Ala Asp Pro Gln
189 Gly Gly Ile Val Leu Ser Leu Leu Gly His Leu Arg Leu Cys Lys Arg
191 Leu His Ser Glu Pro Asp Gly Glu Gly Pro Glu Lys Ile His Val Ala
193 Gly Ser Ser Ala Pro Met Asp Arg Trp His Ser Pro Gln Gln Lys His
                            295
192
195 Pro Arg Val Arg Gln Arg Pro Asp Pro Glu Lys Leu Cys Gln Glu Gln
197 Met Glu Thr Ser Ile Cys His Gly Arg Arg Glu Thr Tyr Glu Lys Thr
199 Thr Pro Arg Gln Gln Pro Gly Gln Phe Lys Cys Lys Cys Phe Glu Gln
 201 Pro Gln Phe Gly Gln Pro Lys Arg Leu Cys Val Cys Ser Lys Thr Arg
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         370
 203 Ile Pro Gln Leu
 204 385
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 208 <211> LENGTH: 1074
 209 <212> TYPE: DNA
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 214 aagatetteg agtteaaaga gaeeetegga accggggeet ttteegaagt ggttttaget 120
 215 gaagagaagg caactggcaa gctctttgct gtgaagtgta tccctaagaa ggcgctgaag 180
  216 ggcaaggaaa gcagcataga gaatgagata gccgtcctga gaaagattaa gcatgaaaat 240
  217 attgttgccc tggaagacat ttatgaaagc ccaaatcacc tgtacttggt catgcagctg 300
  218 gtgtccggtg gagagctgtt tgaccggata gtggagaagg ggttttatac agagaaggat 360
  219 gccagcactc tgatccgcca agtettggac gccgtgtact atctccacag aatgggcatc 420
  220 gtccacagag acctcaagcc cgaaaatctc ttgtactaca gtcaagatga ggagtccaaa 480
  221 ataatgatca gtgactttgg attgtcaaaa atggagggca aaggagatgt gatgtccact 540
  222 gcctgtggaa ctccaggcta tgtcgctcct gaagtcctcg cccagaaacc ttacagcaaa 600
  223 gccgttgact gctggtccat cggagtgatt gcctacatct tgctctgcgg ctaccctcct 660
  224 ttttatgatg aaaatgactc caagctcttt gagcagatcc tcaaggcgga atatgagttt 720
  225 gactetecet actgggatga cateteegae tetgeaaaag actteatteg gaacetgatg 780
  226 gagaaggacc cgaataaaag atacacgtgt gagcaggcag ctcggcaccc atggatcgct 840
  227 ggtgacacag coctoaacaa aaacatocac gagtoogtca gcgcccagat ccggaaaaac 900
  228 tttgccaaga gcaaatggag acaagcattt aatgccacgg ccgtcgtgag acatatgaga 960
  229 aaactacacc tcggcagcag cctggacagt tcaaatgcaa gtgtttcgag cagcctcagt 1020
  230 ttggccagcc aaaaagactg tgcgtatgta gcaaaaccag aatccctcag ctga
   232 <210> SEQ ID NO: 4
   233 <211> LENGTH: 3579
   234 <212> TYPE: DNA
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   237 <220> FEATURE:
   238 <221> NAME/KEY: 5'UTR
   239 <222> LOCATION: (1)...(1212)
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RAW SEQUENCE LISTING DATE: 01/15/2002
PATENT APPLICATION: US/10/024,036 TIME: 18:18:40

Input Set : A:\seq list.txt

Output Set: N:\CRF3\01152002\J024036.raw

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245 <222> LOCATION: (3160)...(3579)
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249 ataccatgct gcctgggaaa cagcaagaac tccatcagtg gcagagacta tcactattat 120
250 tacattaaaa acaaccctga tatcaagcca gttgaaaatg gaccttggag ggaaaaagta 180
251 cgagaaacca tgaaggatca agttcagcga aatgaggaca aatctactac cttgaaattg 240
252 gctgattttg gacttgcaaa gcatgtggtg agacctatat ttactgtgtg tgggacccca 300
253 acttacgtag ctcccgaaat tctttctgag aaaggttatg gactggaggt ggacatgtgg 360
254 gctgctggcg tgatcctcta tatcctgctg tgtggctttc ccccattccg cagccctgag 420
255 agggaccagg acgagetett taacateate cagetgggee aetttgagtt cetececeet 480
256 tactgggaca atatctctga tgctgctaaa gatctggtga gccggttgct ggtggtagac 540
257 cccaaaaagc gctacacagc tcatcaggtt cttcagcacc cctggatcga aacagctggc 600
258 aagaccaata cagtgaaacg acagaagcag gtgtccccca gcagcgaggg tcacttccgg 660
259 agccagcaca agagggttgt ggagcaggta tcatatcygc tgagggctca agatgtgtct 720
260 cttaaagccc caaattccca ctcaacttct catagccatt atgactgatt tagctgaata 780
261 accttgggac agcaaggeet atgtgaccat tetetaaaat atttaagete gagaateaca 840
262 gagcggaagc tgcaaggctc ctggctgcct gccagccgag ggaatctgga gaaaccattc 900
263 ctggggccgc gtggccccgt cgtgcccttg ttctgccctc ggaatggcct tcactcagca 960
264 catcctgaga acagecetet gaageceagg gtegtgaeeg tagtgaaget gggtgggeag 1020
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266 ttagctgaca tctcagaagc cttgggctct cccagatgga agaatgaccg tgtgaggaaa 1140
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268 gctttcatag ct atg ggc aaa gaa cca ctg aca ctg aag agc att cag gtg 1251
                  Met Gly Lys Glu Pro Leu Thr Leu Lys Ser Ile Gln Val
269
                                                        10
270
272 gct gta gaa gaa ctg tac ccc aac aaa gcc cgg gcc ctg aca ctg gcc
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273 Ala Val Glu Glu Leu Tyr Pro Asn Lys Ala Arg Ala Leu Thr Leu Ala
276 cag cac age cgt gcc cct tct cca agg ctg agg agc agg ctg ttt agc
                                                                       1347
277 Gln His Ser Arg Ala Pro Ser Pro Arg Leu Arg Ser Arg Leu Phe Ser
278
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280 aag gct ctg aaa gga gac cac cgc tgt ggg gag acc gag acc ccc aag
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281 Lys Ala Leu Lys Gly Asp His Arg Cys Gly Glu Thr Glu Thr Pro Lys
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284 agc tgc agc gaa gtt gca gga tgc aag gca gcc atg agg cac cag ggg
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285 Ser Cys Ser Glu Val Ala Gly Cys Lys Ala Ala Met Arg His Gln Gly
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                  65
288 aag atc ccc gag gag ctt tca cta gat gac aga gcg agg acc cag aag
                                                                        1491
289 Lys Ile Pro Glu Glu Leu Ser Leu Asp Asp Arg Ala Arg Thr Gln Lys
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                                  85
              80
 290
292 aag tgg ggg agg ggg aaa tgg gag cca gaa ccc agt agc aag ccc ccc
                                                                        1539
293 Lys Trp Gly Arg Gly Lys Trp Glu Pro Glu Pro Ser Ser Lys Pro Pro
                                                 105
                             100
 296 agg gaa gcc act ctg gaa gag agg cac gca agg gga gag aag cat ctt
                                                                        1587
 297 Arg Glu Ala Thr Leu Glu Glu Arg His Ala Arg Gly Glu Lys His Leu
                         115
 298 110
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FNI

Use of n and/or Xaa has been detected in the Sequence Listing. Esview the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/024,036

DATE: 01/15/2002 TIME: 18:18:41

Input Set : A:\seq list.txt

Output Set: N:\CRF3\01152002\J024036.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:35 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1

L:35 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 L:656 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 L:709 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8

L:764 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

 $L\!:\!800$  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10